



SEQUENCE LISTING

<110> Kaufman, Randal J.
Tirasophon, Witoon
Welihinda, Ajith A.

<120> Irelp, A NOVEL MAMMALIAN PROTEIN AND GENE ENCODING SAME

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<150> 60/093,526

<151> 1998-07-21

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<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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Met Pro Ala Arg Arg Leu
1 5

ctg ctg ctg ctg acg ctg ctg ctg ccc ggc ctc ggg att ttt gga agt 162
Leu Leu Leu Leu Thr Leu Leu Leu Pro Gly Leu Gly Ile Phe Gly Ser
10 15 20

acc agc aca gtg acg ctt cct gaa acc ttg ttg ttt gtg tca acg ctg 210
Thr Ser Thr Val Thr Leu Pro Glu Thr Leu Leu Phe Val Ser Thr Leu
25 30 35

gat gga agt ttg cat gct gtc agc aag agg aca ggc tca atc aaa tgg 258
Asp Gly Ser Leu His Ala Val Ser Lys Arg Thr Gly Ser Ile Lys Trp
40 45 50

act tta aaa gaa gat cca gtc ctg cag gtc cca aca cat gtg gaa gag 306
Thr Leu Lys Glu Asp Pro Val Leu Gln Val Pro Thr His Val Glu Glu
55 60 65 70

cct gcc ttt ctc cca gat cct aat gat ggc agc ctg tat acg ctt gga 354
Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly Ser Leu Tyr Thr Leu Gly

TECH CENTER 1600/2900

APR 13 2001

RECEIVED

75										80					85					
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ggc	aaa	aag	cag	gac	atc	tgg	tat	gtt	att	gac	ctc	ctg	acc	gga	gag	498				
Gly	Lys	Lys	Gln	Asp	Ile	Trp	Tyr	Val	Ile	Asp	Leu	Leu	Thr	Gly	Glu					
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aag	cag	cag	act	ttg	tca	tgc	gcc	ttt	gca	gat	agt	ctc	tgc	cca	tca	546				
Lys	Gln	Gln	Thr	Leu	Ser	Ser	Ala	Phe	Ala	Asp	Ser	Leu	Cys	Pro	Ser					
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Thr	Ser	Leu	Leu	Tyr	Leu	Gly	Arg	Thr	Glu	Tyr	Thr	Ile	Thr	Met	Tyr					
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gcg	gcc	tca	ctg	cct	gag	gac	gaa	ggg	gac	tac	aag	atg	tcc	cac	ttt	690				
Ala	Ala	Ser	Leu	Pro	Glu	Asp	Glu	Gly	Asp	Tyr	Lys	Met	Ser	His	Phe					
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Val	Trp	Gln	Arg	Glu	Gly	Leu	Arg	Lys	Val	Met	His	Ile	Asn	Val	Ala					
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Asp Pro Gly Leu Lys Ser Lys Asn Lys Leu Asn Tyr Leu Arg Asn Tyr	
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Trp Leu Leu Ile Gly His His Glu Thr Pro Leu Ser Ala Ser Thr Lys	
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Ile Pro Ala Asp Ser Glu Lys Lys Ser Phe Glu Glu Val Ile Asn Leu	
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Val Asp Gln Thr Ser Glu Asn Ala Pro Thr Thr Val Ser Arg Asp Val	
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Glu Glu Lys Pro Ala His Ala Pro Ala Arg Pro Glu Ala Pro Val Asp	
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Ser Met Leu Lys Asp Met Ala Thr Ile Ile Leu Ser Thr Phe Leu Leu	
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Ile Gly Trp Val Ala Phe Ile Ile Thr Tyr Pro Leu Ser Met His Gln	
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Gln Gln Gln Leu Gln His Gln Gln Phe Gln Lys Glu Leu Glu Lys Ile	
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Gln Leu Leu Gln Gln Gln Gln Gln Gln Leu Pro Phe His Pro Pro Gly	
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Asp Thr Ala Gln Asp Gly Glu Leu Leu Asp Thr Ser Gly Pro Tyr Ser	
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Glu Ser Ser Gly Thr Ser Ser Pro Ser Thr Ser Pro Arg Ala Ser Asn	
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His Ser Leu Cys Ser Gly Ser Ser Ala Ser Lys Ala Gly Ser Ser Pro	
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Gly Lys Ile Ser Phe Cys Pro Lys Asp Val Leu Gly His Gly Ala Glu	
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Gly Thr Ile Val Tyr Arg Gly Met Phe Asp Asn Arg Asp Val Ala Val	
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Lys Arg Ile Leu Pro Glu Cys Phe Ser Phe Ala Asp Arg Glu Val Gln	
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Leu Leu Arg Glu Ser Asp Glu His Pro Asn Val Ile Arg Tyr Phe Cys	
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Thr Glu Lys Asp Arg Gln Phe Gln Tyr Ile Ala Ile Glu Leu Cys Ala	
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Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys Asp Phe Ala His Leu Gly	
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Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr Thr Ser Gly Leu Ala His	
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Leu His Ser Leu Asn Ile Val His Arg Asp Leu Lys Pro His Asn Ile	
680 685 690	
ctc ata tcc atg ccc aat gca cac ggc aag atc aag gcc atg atc tcc	2226
Leu Ile Ser Met Pro Asn Ala His Gly Lys Ile Lys Ala Met Ile Ser	
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cgc cga tct ggg gtg cct ggc aca gaa ggc tgg atc gct cca gag atg	2322
Arg Arg Ser Gly Val Pro Gly Thr Glu Gly Trp Ile Ala Pro Glu Met	
730 735 740	
ctg agc gaa gac tgt aag gag aac cct acc tac acg gtg gac atc ttt	2370
Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr Tyr Thr Val Asp Ile Phe	
745 750 755	
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Ser	Ala	Gly	Cys	Val	Phe	Tyr	Val	Val	Ser	Glu	Gly	Ser	His	Pro		
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Arg	Lys	Phe	Arg	Thr	Tyr	Lys	Gly	Gly	Ser	Val	Arg	Asp	Leu	Leu	Arg	
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Ser	Arg	Phe	Pro	His	Leu	Leu	Ala	His	Thr	Tyr	Arg	Ala	Met	Glu	Leu	
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Cys	Ser	His	Glu	Arg	Leu	Phe	Gln	Pro	Tyr	Tyr	Phe	His	Glu	Pro	Pro	
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 ccggaattga gaggtggggg atgctgagga gggggaggac ggagttcaga ggggtgtcgtc 3527
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<211> 977

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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Leu Phe Val Ser Thr Leu Asp Gly Ser Leu His Ala Val Ser Lys Arg
 35 40 45

Thr Gly Ser Ile Lys Trp Thr Leu Lys Glu Asp Pro Val Leu Gln Val
 50 55 60

Pro Thr His Val Glu Glu Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly
 65 70 75 80

Ser Leu Tyr Thr Leu Gly Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu
 85 90 95

Pro Phe Thr Ile Pro Glu Leu Val Gln Ala Ser Pro Cys Arg Ser Ser
 100 105 110

Asp Gly Ile Leu Tyr Met Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile
 115 120 125

Asp Leu Leu Thr Gly Glu Lys Gln Gln Thr Leu Ser Ser Ala Phe Ala
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Asp Ser Leu Cys Pro Ser Thr Ser Leu Leu Tyr Leu Gly Arg Thr Glu
 145 150 155 160

Tyr Thr Ile Thr Met Tyr Asp Thr Lys Thr Arg Glu Leu Arg Trp Asn
165 170 175

Ala Thr Tyr Phe Asp Tyr Ala Ala Ser Leu Pro Glu Asp Glu Gly Asp
180 185 190

Tyr Lys Met Ser His Phe Val Ser Asn Gly Asp Gly Leu Val Val Thr
195 200 205

Val Asp Ser Glu Ser Gly Asp Val Leu Trp Ile Gln Asn Tyr Ala Ser
210 215 220

Pro Val Val Ala Phe Tyr Val Trp Gln Arg Glu Gly Leu Arg Lys Val
225 230 235 240

Met His Ile Asn Val Ala Val Glu Thr Leu Arg Tyr Leu Thr Phe Met
245 250 255

Ser Gly Glu Val Gly Arg Ile Thr Lys Trp Lys Tyr Pro Phe Pro Lys
260 265 270

Glu Thr Glu Ala Lys Ser Lys Leu Thr Pro Thr Leu Tyr Val Gly Lys
275 280 285

Tyr Ser Thr Ser Leu Tyr Ala Ser Pro Ser Met Val His Glu Gly Val
290 295 300

Ala Val Val Pro Arg Gly Ser Thr Leu Pro Leu Leu Glu Gly Pro Gln
305 310 315 320

Thr Asp Gly Val Thr Ile Gly Asp Lys Gly Glu Cys Val Ile Thr Pro
325 330 335

Ser Thr Asp Val Lys Phe Asp Pro Gly Leu Lys Ser Lys Asn Lys Leu
340 345 350

Asn Tyr Leu Arg Asn Tyr Trp Leu Leu Ile Gly His His Glu Thr Pro
355 360 365

Leu Ser Ala Ser Thr Lys Met Leu Glu Arg Phe Pro Asn Asn Leu Pro
370 375 380

Lys His Arg Glu Asn Val Ile Pro Ala Asp Ser Glu Lys Lys Ser Phe
385 390 395 400

Glu Glu Val Ile Asn Leu Val Asp Gln Thr Ser Glu Asn Ala Pro Thr
405 410 415

Thr Val Ser Arg Asp Val Glu Glu Lys Pro Ala His Ala Pro Ala Arg
420 425 430

Pro Glu Ala Pro Val Asp Ser Met Leu Lys Asp Met Ala Thr Ile Ile
435 440 445

Leu Ser Thr Phe Leu Leu Ile Gly Trp Val Ala Phe Ile Ile Thr Tyr
450 455 460

Pro Leu Ser Met His Gln Gln Gln Gln Leu Gln His Gln Gln Phe Gln
465 470 475 480

Lys Glu Leu Glu Lys Ile Gln Leu Leu Gln Gln Gln Gln Gln Leu
485 490 495

Pro Phe His Pro Pro Gly Asp Thr Ala Gln Asp Gly Glu Leu Leu Asp
500 505 510

Thr Ser Gly Pro Tyr Ser Glu Ser Ser Gly Thr Ser Ser Pro Ser Thr
515 520 525

Ser Pro Arg Ala Ser Asn His Ser Leu Cys Ser Gly Ser Ser Ala Ser
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Lys Ala Gly Ser Ser Pro Ser Leu Glu Gln Asp Asp Gly Asp Glu Glu
545 550 555 560

Thr Ser Val Val Ile Val Gly Lys Ile Ser Phe Cys Pro Lys Asp Val
565 570 575

Leu Gly His Gly Ala Glu Gly Thr Ile Val Tyr Arg Gly Met Phe Asp
580 585 590

Asn Arg Asp Val Ala Val Lys Arg Ile Leu Pro Glu Cys Phe Ser Phe
595 600 605

Ala Asp Arg Glu Val Gln Leu Leu Arg Glu Ser Asp Glu His Pro Asn
610 615 620

Val Ile Arg Tyr Phe Cys Thr Glu Lys Asp Arg Gln Phe Gln Tyr Ile
625 630 635 640

Ala Ile Glu Leu Cys Ala Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys
645 650 655

Asp Phe Ala His Leu Gly Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr
660 665 670

Thr Ser Gly Leu Ala His Leu His Ser Leu Asn Ile Val His Arg Asp
675 680 685

Leu Lys Pro His Asn Ile Leu Ile Ser Met Pro Asn Ala His Gly Lys
690 695 700

Ile Lys Ala Met Ile Ser Asp Phe Gly Leu Cys Lys Lys Leu Ala Val
705 710 715 720

Gly Arg His Ser Phe Ser Arg Arg Ser Gly Val Pro Gly Thr Glu Gly
725 730 735

Trp Ile Ala Pro Glu Met Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr
740 745 750

Tyr Thr Val Asp Ile Phe Ser Ala Gly Cys Val Phe Tyr Tyr Val Val
755 760 765

Ser Glu Gly Ser His Pro Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn
770 775 780

Ile Leu Leu Gly Ala Cys Ser Leu Asp Cys Leu His Pro Glu Lys His
785 790 795 800

Glu Asp Val Ile Ala Arg Glu Leu Ile Glu Lys Met Ile Ala Met Asp
805 810 815

Pro Gln Lys Arg Pro Ser Ala Asn Asp Val Leu Lys His Pro Phe Phe
820 825 830

Trp Ser Leu Glu Lys Gln Leu Gln Phe Phe Gln Asp Val Ser Asp Arg
835 840 845

Ile Glu Lys Glu Ser Leu Asp Gly Pro Ile Val Lys Gln Leu Glu Arg
850 855 860

Gly Gly Arg Ala Val Val Lys Met Asp Trp Arg Glu Asn Ile Thr Asp
865 870 875 880

Pro Leu Gln Thr Asp Leu Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser
885 890 895

Val Arg Asp Leu Leu Arg Ala Met Arg Asn Lys Lys His His Tyr Arg
900 905 910

Glu Leu Pro Ala Glu Val Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp
915 920 925

Phe Val Cys Tyr Phe Thr Ser Arg Phe Pro His Leu Leu Ala His Thr
930 935 940

Tyr Arg Ala Met Glu Leu Cys Ser His Glu Arg Leu Phe Gln Pro Tyr
945 950 955 960

Tyr Phe His Glu Pro Pro Glu Pro Gln Pro Pro Val Thr Pro Asp Ala
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Leu

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<211> 977

<212> PRT

<213> Homo sapiens

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20 25 30

Leu Phe Val Ser Thr Leu Asp Gly Ser Leu His Ala Val Ser Lys Arg

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Ser	Leu	Tyr	Thr	Leu	Gly	Ser	Lys	Asn	Asn	Glu	Gly	Leu	Thr	Lys	Leu
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Pro	Phe	Thr	Ile	Pro	Glu	Leu	Val	Gln	Ala	Ser	Pro	Cys	Arg	Ser	Ser
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Tyr	Thr	Ile	Thr	Met	Tyr	Asp	Thr	Lys	Thr	Arg	Glu	Leu	Arg	Trp	Asn
				165					170					175	
Ala	Thr	Tyr	Phe	Asp	Tyr	Ala	Ala	Ser	Leu	Pro	Glu	Asp	Glu	Gly	Asp
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Tyr	Lys	Met	Ser	His	Phe	Val	Ser	Asn	Gly	Asp	Gly	Leu	Val	Val	Thr
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	210					215					220				
Pro	Val	Val	Ala	Phe	Tyr	Val	Trp	Gln	Arg	Glu	Gly	Leu	Arg	Lys	Val
225						230					235				240
Met	His	Ile	Asn	Val	Ala	Val	Glu	Thr	Leu	Arg	Tyr	Leu	Thr	Phe	Met
				245					250					255	
Ser	Gly	Glu	Val	Gly	Arg	Ile	Thr	Lys	Trp	Lys	Tyr	Pro	Phe	Pro	Lys
			260					265					270		
Glu	Thr	Glu	Ala	Lys	Ser	Lys	Leu	Thr	Pro	Thr	Leu	Tyr	Val	Gly	Lys
			275				280					285			
Tyr	Ser	Thr	Ser	Leu	Tyr	Ala	Ser	Pro	Ser	Met	Val	His	Glu	Gly	Val
	290					295					300				
Ala	Val	Val	Pro	Arg	Gly	Ser	Thr	Leu	Pro	Leu	Leu	Glu	Gly	Pro	Gln
305						310					315				320
Thr	Asp	Gly	Val	Thr	Ile	Gly	Asp	Lys	Gly	Glu	Cys	Val	Ile	Thr	Pro
			325						330					335	
Ser	Thr	Asp	Val	Lys	Phe	Asp	Pro	Gly	Leu	Lys	Ser	Lys	Asn	Lys	Leu

340							345					350				
Asn	Tyr	Leu	Arg	Asn	Tyr	Trp	Leu	Leu	Ile	Gly	His	His	Glu	Thr	Pro	
		355					360					365				
Leu	Ser	Ala	Ser	Thr	Lys	Met	Leu	Glu	Arg	Phe	Pro	Asn	Asn	Leu	Pro	
		370				375					380					
Lys	His	Arg	Glu	Asn	Val	Ile	Pro	Ala	Asp	Ser	Glu	Lys	Lys	Ser	Phe	
385					390					395					400	
Glu	Glu	Val	Ile	Asn	Leu	Val	Asp	Gln	Thr	Ser	Glu	Asn	Ala	Pro	Thr	
				405					410					415		
Thr	Val	Ser	Arg	Asp	Val	Glu	Glu	Lys	Pro	Ala	His	Ala	Pro	Ala	Arg	
			420					425					430			
Pro	Glu	Ala	Pro	Val	Asp	Ser	Met	Leu	Lys	Asp	Met	Ala	Thr	Ile	Ile	
		435					440					445				
Leu	Ser	Thr	Phe	Leu	Leu	Ile	Gly	Trp	Val	Ala	Phe	Ile	Ile	Thr	Tyr	
		450				455					460					
Pro	Leu	Ser	Met	His	Gln	Gln	Gln	Gln	Leu	Gln	His	Gln	Gln	Phe	Gln	
465					470					475					480	
Lys	Glu	Leu	Glu	Lys	Ile	Gln	Leu	Leu	Gln	Gln	Gln	Gln	Gln	Gln	Leu	
				485					490					495		
Pro	Phe	His	Pro	Pro	Gly	Asp	Thr	Ala	Gln	Asp	Gly	Glu	Leu	Leu	Asp	
			500					505					510			
Thr	Ser	Gly	Pro	Tyr	Ser	Glu	Ser	Ser	Gly	Thr	Ser	Ser	Pro	Ser	Thr	
		515					520					525				
Ser	Pro	Arg	Ala	Ser	Asn	His	Ser	Leu	Cys	Ser	Gly	Ser	Ser	Ala	Ser	
---		530	---			535	---				540	---			---	
Lys	Ala	Gly	Ser	Ser	Pro	Ser	Leu	Glu	Gln	Asp	Asp	Gly	Asp	Glu	Glu	
545					550					555					560	
Thr	Ser	Val	Val	Ile	Val	Gly	Lys	Ile	Ser	Phe	Cys	Pro	Lys	Asp	Val	
				565					570					575		
Leu	Gly	His	Gly	Ala	Glu	Gly	Thr	Ile	Val	Tyr	Arg	Gly	Met	Phe	Asp	
			580					585					590			
Asn	Arg	Asp	Val	Ala	Val	Lys	Arg	Ile	Leu	Pro	Glu	Cys	Phe	Ser	Phe	
		595					600					605				
Ala	Asp	Arg	Glu	Val	Gln	Leu	Leu	Arg	Glu	Ser	Asp	Glu	His	Pro	Asn	
		610				615					620					
Val	Ile	Arg	Tyr	Phe	Cys	Thr	Glu	Lys	Asp	Arg	Gln	Phe	Gln	Tyr	Ile	
625					630					635					640	
Ala	Ile	Glu	Leu	Cys	Ala	Ala	Thr	Leu	Gln	Glu	Tyr	Val	Glu	Gln	Lys	

				645				650				655				
Asp	Phe	Ala	His	Leu	Gly	Leu	Glu	Pro	Ile	Thr	Leu	Leu	Gln	Gln	Thr	
				660					665					670		
Thr	Ser	Gly	Leu	Ala	His	Leu	His	Ser	Leu	Asn	Ile	Val	His	Arg	Asp	
				675					680					685		
Leu	Lys	Pro	His	Asn	Ile	Leu	Ile	Ser	Met	Pro	Asn	Ala	His	Gly	Lys	
				690					695					700		
Ile	Lys	Ala	Met	Ile	Ser	Asp	Phe	Gly	Leu	Cys	Lys	Lys	Leu	Ala	Val	
				705					710					715		
Gly	Arg	His	Ser	Phe	Ser	Arg	Arg	Ser	Gly	Val	Pro	Gly	Thr	Glu	Gly	
				725					730					735		
Trp	Ile	Ala	Pro	Glu	Met	Leu	Ser	Glu	Asp	Cys	Lys	Glu	Asn	Pro	Thr	
				740					745					750		
Tyr	Thr	Val	Asp	Ile	Phe	Ser	Ala	Gly	Cys	Val	Phe	Tyr	Tyr	Val	Val	
				755					760					765		
Ser	Glu	Gly	Ser	His	Pro	Phe	Gly	Lys	Ser	Leu	Gln	Arg	Gln	Ala	Asn	
				770					775					780		
Ile	Leu	Leu	Gly	Ala	Cys	Ser	Leu	Asp	Cys	Leu	His	Pro	Glu	Lys	His	
				785					790					795		
Glu	Asp	Val	Ile	Ala	Arg	Glu	Leu	Ile	Glu	Lys	Met	Ile	Ala	Met	Asp	
				805					810					815		
Pro	Gln	Lys	Arg	Pro	Ser	Ala	Asn	Asp	Val	Leu	Lys	His	Pro	Phe	Phe	
				820					825					830		
Trp	Ser	Leu	Glu	Lys	Gln	Leu	Gln	Phe	Phe	Gln	Asp	Val	Ser	Asp	Arg	
				835					840					845		
Ile	Glu	Lys	Glu	Ser	Leu	Asp	Gly	Pro	Ile	Val	Lys	Gln	Leu	Glu	Arg	
				850					855					860		
Gly	Gly	Arg	Ala	Val	Val	Lys	Met	Asp	Trp	Arg	Glu	Asn	Ile	Thr	Asp	
				865					870					875		
Pro	Leu	Gln	Thr	Asp	Leu	Arg	Lys	Phe	Arg	Thr	Tyr	Lys	Gly	Gly	Ser	
				885					890					895		
Val	Arg	Asp	Leu	Leu	Arg	Ala	Met	Arg	Asn	Lys	Lys	His	His	Tyr	Arg	
				900					905					910		
Glu	Leu	Pro	Ala	Glu	Val	Arg	Glu	Thr	Leu	Gly	Thr	Leu	Pro	Asp	Asp	
				915					920					925		
Phe	Val	Cys	Tyr	Phe	Thr	Ser	Arg	Phe	Pro	His	Leu	Leu	Ala	His	Thr	
				930					935					940		
Tyr	Arg	Ala	Met	Glu	Leu	Cys	Ser	His	Glu	Arg	Leu	Phe	Gln	Pro	Tyr	

His Tyr Ala Ser Ser Ser His Gly Tyr Ile Leu Thr Phe Asp Arg Glu
225 230 235 240

Thr Gly Glu Met Arg Trp Glu Gln Asp Leu Lys Gln Pro Val Val Ala
245 250 255

Leu Tyr Leu Leu Arg Asp Asp Gly Leu His Lys Leu Pro Phe Glu Val
260 265 270

Met Gly Lys Glu Thr Met Glu Asn Val Ala Lys Asn Ile Phe Thr Val
275 280 285

Asp Gln Trp Pro Thr Val Leu Gly Val Asn Ala Ala Asp Pro Gln Thr
290 295 300

Thr Ser Leu Thr Asn Gln Phe Phe Pro Ala Leu Phe Val Gly Glu Ser
305 310 315 320

Ser Phe Gly Leu Tyr Ala Ile Glu Ala Leu Val Asp His Gln Thr Ile
325 330 335

Thr Tyr Ser Pro Lys Leu Leu Gly Pro Pro Leu Leu Glu Gly Pro Ala
340 345 350

Pro Ile Ala Leu Thr Glu Met Glu Lys Glu Glu Tyr Leu Pro Pro Arg
355 360 365

Arg Pro Ile Ile Arg Asn Ile Pro Pro Ser Ile Thr His Lys Thr Ser
370 375 380

Asp Gly Glu Tyr Leu Leu Leu Gly Tyr His Asp Arg Pro Met Met Thr
385 390 395 400

Met Ala Thr Ile Ile Pro Thr Arg Tyr Pro Val Pro Gly Pro His Lys
405 410 415

~~Ala Ile Gly Ser Thr Ile Glu Arg Pro Pro Pro Gln Leu Leu Gly Pro~~
~~420 425 430~~

Val Glu Pro Gln Lys His Glu Asp Thr Ser Phe Ile Leu Leu Leu Leu
435 440 445

Asn Asn His Pro Ile Pro Phe Tyr Ala Thr Leu Val Thr Met Phe Ala
450 455 460

Leu Leu Leu Thr Val Ile Trp Gln Cys Gly Arg Gln Trp Asp Gln Gln
465 470 475 480

Lys Ser Thr Ser Arg Met Asp Ser Phe Glu Ile Val Asn Asn Pro Gly
485 490 495

Glu Ser Arg Ser Ala Gln Thr Ser Lys Gln Ser Asn Arg Gly Ser Phe
500 505 510

Gly Trp Ala Asn Arg Lys Ile Glu Ile Pro Glu Gly Trp Met Ala Val
515 520 525

Gly Ser Lys Leu Met Tyr Ser Pro Ser Asp Ile Leu Gly Thr Gly Cys
530 535 540

Glu Gly Thr Val Val Tyr Arg Gly Thr Phe Asp Gly Arg Glu Val Ala
545 550 555 560

Val Lys Arg Val Val Ser Glu Phe Val Lys Phe Ala His Arg Glu Ala
565 570 575

Asp Leu Leu Arg Glu Ser Asp Thr His Pro His Val Ile Arg Tyr Phe
580 585 590

Cys Met Glu Ser Asp Ser Gln Phe Arg Tyr Leu Ala Leu Glu Leu Cys
595 600 605

Ile Ala Ser Leu Asn Asp Tyr Val Glu Gln Lys Glu Val Gln Gln Asn
610 615 620

Val Thr Ile Ala Leu Arg Asp Ile Met Lys Gln Ala Thr Asp Gly Leu
625 630 635 640

Ala His Leu His Ala Ser Lys Ile Val His Arg Asp Met Lys Pro Gln
645 650 655

Asn Val Leu Ile Thr Met Ala Ser Gln Arg Gly Glu Met Arg Ala Val
660 665 670

Ile Ser Asp Phe Gly Leu Cys Lys Arg Val Gln Pro Gly Lys Asn Ser
675 680 685

Ile Ser Arg Gly Ile Ala Ser Gly Leu Ala Gly Thr Asp Gly Trp Ile
690 695 700

Ala Pro Glu Val Leu Ile Ser Ala Ser Thr Ser Tyr Pro Val Asp Ile
705 710 715 720

~~Phe Ser Leu Gly Cys Ile Phe Tyr Tyr Val Leu Thr Ser Gly Thr His~~
~~725 730 735~~

Pro Phe Gly Lys Ser Leu His Arg Gln Ala Asn Ile Val Asn Gly Glu
740 745 750

Tyr Thr Leu Asn Lys Leu Ala Asp Leu Asp Asp Trp Ser Leu Ala Asp
755 760 765

Asp Leu Ile Ser Ser Met Leu Asn Val Glu Pro Leu His Arg Leu Thr
770 775 780

Ala Asp Ala Val Leu Asn His Pro Phe Phe Trp Thr Ser Glu Lys Arg
785 790 795 800

Leu Ala Tyr Phe Ser Asp Val Ser Asp Arg Val Glu Lys Glu Glu Asp
805 810 815

Asn Ser Pro Val Val Arg Arg Ile Glu Thr Asp Ala Arg Ile Val Val
820 825 830

Cys Gly Gly Trp Arg Glu Lys Ile Cys Asp Ala Leu Lys Glu Asp Leu
 835 840 845
 Arg Lys Phe Arg Thr Tyr Lys Ser Phe Ser Val Arg Asp Leu Leu Arg
 850 855 860
 Ala Met Arg Asn Lys Lys His His Tyr Arg Glu Leu Pro Glu Asp Val
 865 870 875 880
 Arg Gln Ser Leu Gly Asp Ile Pro Asp Gln Phe Leu His Tyr Phe Thr
 885 890 895
 Ser Arg Phe Pro Arg Leu Leu Leu His Val Tyr Lys Ala Thr Glu Tyr
 900 905 910
 Cys Ser Gly Glu Ala Val Phe Lys Arg Tyr Tyr Ser Asp Asp Val Arg
 915 920 925
 Ala Arg Met Tyr Pro Ile Val Glu Glu Glu Glu Arg Val Arg Lys Lys
 930 935 940
 Ile Lys Glu Glu Met Ala Asn Glu Val Trp Ala Arg Ala Pro Lys Pro
 945 950 955 960
 Val Glu Gln Arg Thr Pro Leu Lys Leu Asp Lys Arg Asn Ile Lys Lys
 965 970 975
 Lys Ser Asn Pro Asn Thr Asp
 980

<210> 5
 <211> 443
 <212> PRT
 <213> *Saccharomyces cerevisiae*

~~<400> 5~~
 Leu Val Val Ser Cys Lys Ile Leu Gly Tyr Gly Ser Ser Gly Thr Val
 1 5 10 15
 Val Phe Gln Gly Ser Phe Gln Gly Arg Pro Val Ala Val Lys Arg Met
 20 25 30
 Leu Ile Asp Phe Cys Asp Ile Ala Leu Met Glu Ile Lys Leu Leu Thr
 35 40 45
 Glu Ser Asp Asp His Pro Asn Val Ile Arg Tyr Tyr Cys Ser Glu Thr
 50 55 60
 Thr Asp Arg Phe Leu Tyr Ile Ala Leu Glu Leu Cys Asn Leu Asn Leu
 65 70 75 80
 Gln Asp Leu Val Glu Ser Lys Asn Val Ser Asp Glu Asn Leu Lys Leu
 85 90 95
 Gln Lys Glu Tyr Asn Pro Ile Ser Leu Leu Arg Gln Ile Ala Ser Gly
 100 105 110

Val Ala His Leu His Ser Leu Lys Ile Ile His Arg Asp Leu Lys Pro
115 120 125

Gln Asn Ile Leu Val Ser Thr Ser Ser Arg Phe Thr Ala Asp Gln Gln
130 135 140

Thr Gly Ala Glu Asn Leu Arg Ile Leu Ile Ser Asp Phe Gly Leu Cys
145 150 155 160

Lys Lys Leu Asp Ser Gly Gln Ser Ser Phe Arg Thr Asn Leu Asn Asn
165 170 175

Pro Ser Gly Thr Ser Gly Trp Arg Ala Pro Glu Leu Leu Glu Glu Ser
180 185 190

Asn Asn Leu Gln Cys Gln Val Glu Thr Glu His Ser Ser Ser Arg His
195 200 205

Thr Val Val Ser Ser Asp Ser Phe Tyr Asp Pro Phe Thr Lys Arg Arg
210 215 220

Leu Thr Arg Ser Ile Asp Ile Phe Ser Met Gly Cys Val Phe Tyr Tyr
225 230 235 240

Ile Leu Ser Lys Gly Lys His Pro Phe Gly Asp Lys Tyr Ser Arg Glu
245 250 255

Ser Asn Ile Ile Arg Gly Ile Phe Ser Leu Asp Glu Met Lys Cys Leu
260 265 270

His Asp Arg Ser Leu Ile Ala Glu Ala Thr Asp Leu Ile Ser Gln Met
275 280 285

Ile Asp His Asp Pro Leu Lys Arg Pro Thr Ala Met Lys Val Leu Arg
290 295 300

His Pro Leu Phe Trp Pro Lys Ser Lys Lys Leu Glu Phe Leu Leu Lys
305 310 315 320

Val Ser Asp Arg Leu Glu Ile Glu Asn Arg Asp Pro Pro Ser Ala Leu
325 330 335

Leu Met Lys Phe Asp Ala Gly Ser Asp Phe Val Ile Pro Ser Gly Asp
340 345 350

Trp Thr Val Lys Phe Asp Lys Thr Phe Met Asp Asn Leu Glu Arg Tyr
355 360 365

Arg Lys Tyr His Ser Ser Lys Leu Met Asp Leu Leu Arg Ala Leu Arg
370 375 380

Asn Lys Tyr His His Phe Met Asp Leu Pro Glu Asp Ile Ala Glu Leu
385 390 395 400

Met Gly Pro Val Pro Asp Gly Phe Tyr Asp Tyr Phe Thr Lys Arg Phe
405 410 415

Pro Asn Leu Leu Ile Gly Val Tyr Met Ile Val Lys Glu Asn Leu Ser
420 425 430

Asp Asp Gln Ile Leu Arg Glu Phe Leu Tyr Ser
435 440

<210> 6
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
Ile Ser Asp Phe Gly Leu Cys Lys
1 5

<210> 7
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
cgccatgcc

9

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> N at position 1 may be Thymine or Cytosine

<220>
<223> N at positions 4, 9, 13 and 16 may be Adenine or
Guanine

<220>
<223> N at positions 7, 10, 19 and 22 may be any
nucleotide

<220>
<223> N at position 21 may be Adenine or Thymine

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
nttncntntnn ccnaantcng nnat

24

<210> 9
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
Ile Ser Asp Phe Gly Leu Cys Lys
1 5

<210> 10
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
gctctagaac catgccggcc cggcggct 28

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
aggctg~~ccat~~ cattaggat~~e-t~~ 21

<210> 12
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
cattgatgtg catcaccttc ctc 23

<210> 13
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

cggaattcat cacctatccc ctgagcatg

29

<210> 14

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 14

cggaattctc agagggcgtc tggagtca

28